



MRC  
Biostatistics  
Unit



UNIVERSITY OF  
CAMBRIDGE

# Non-monotonic power in Bayesian dynamic borrowing: insights and practical remedies

**Gianmarco Caruso\*** and Pavel Mozgunov

PSI 2025 conference, Wembley Stadium, London, UK  
June 11, 2025

\*[gianmarco.caruso@mrc-bsu.cam.ac.uk](mailto:gianmarco.caruso@mrc-bsu.cam.ac.uk)

# Motivation: non-inferiority oncology trial

RCT to compare two different therapies for treating a cancer that originates in the appendix:

- High-dose regimen (“Dutch protocol”, most used)
- Low-dose regimen (cheaper and *safer*, used in the UK centre)

Can we conclude that the low dose is  
**not less effective** than high dose?

Endpoint: **2-year disease-free survival (DFS)**

$$Y_j \sim \text{Bernoulli}(p_j), \quad j = \{High, Low\}$$

with Bayesian priors on survival rates  $p_j$ 's based on historical data

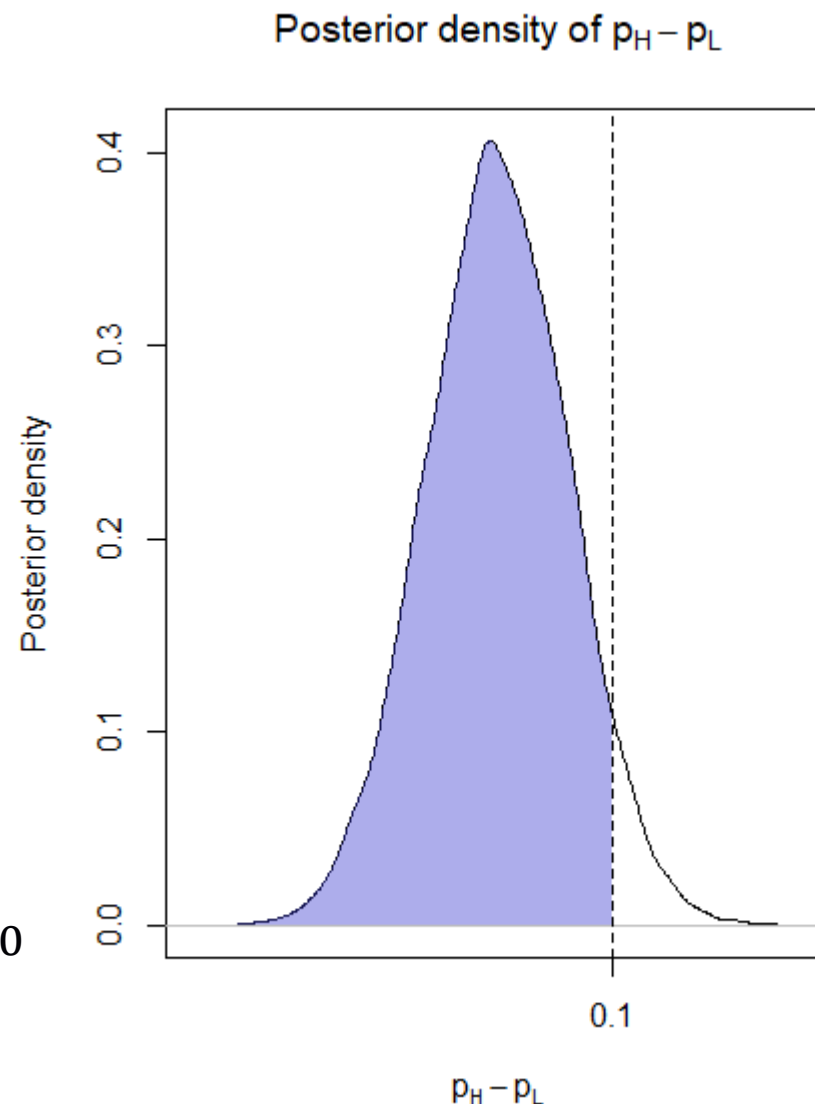
# Bayesian decision-making

## Hypotheses of non-inferiority trial:

- $H_0$  : Difference in survival rates ( $p_H - p_L$ ) is **larger or equal to 0.1 (low-dose is inferior)**
- $H_1$  : Difference in survival rates ( $p_H - p_L$ ) is **smaller than 0.1 (low-dose is not inferior)**

We claim non-inferiority of low-dose regimen if  $P(p_H - p_L < 0.1 | data) > \xi$

N.B.  $\xi$  calibrated to control type I error under specific  $H_0$

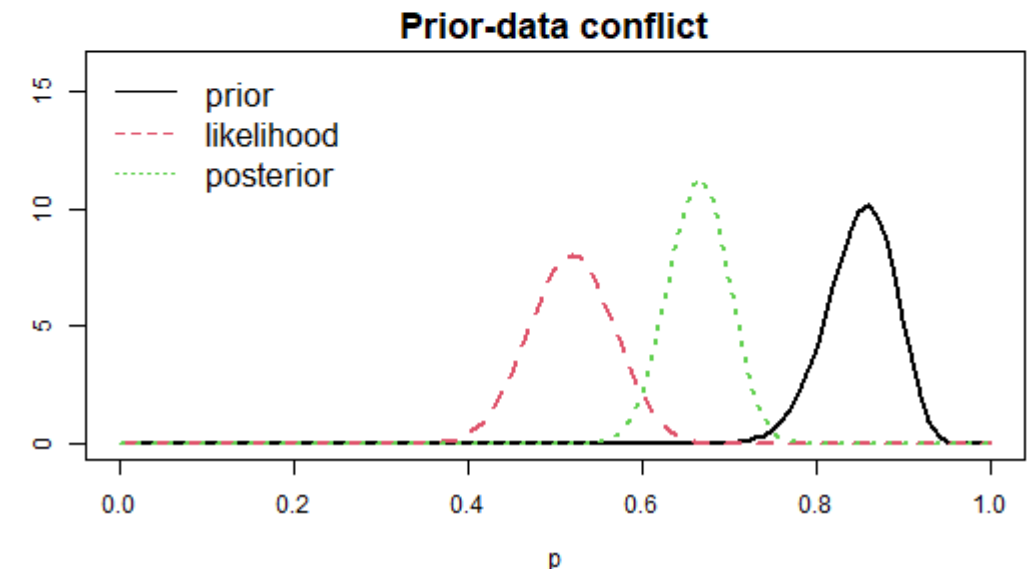
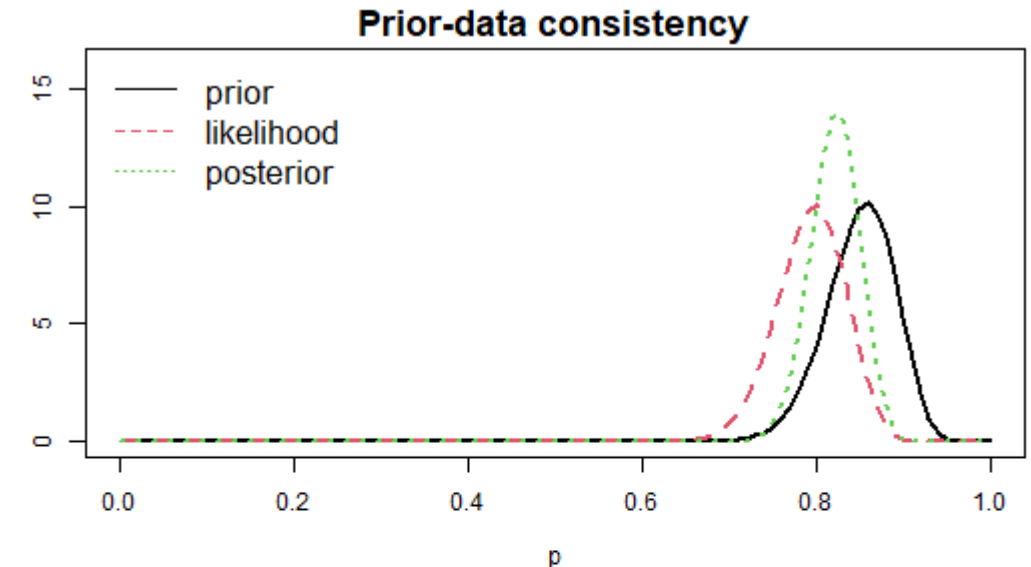


# Prior elicitation from historical data

Prior distributions based on historical survival rates and degree of relevance of past studies (conjugate Beta, MAP, etc.)

**Benefit:** If new and past study data are **consistent**, we gain **efficiency** (=smaller sample size to achieve same power)

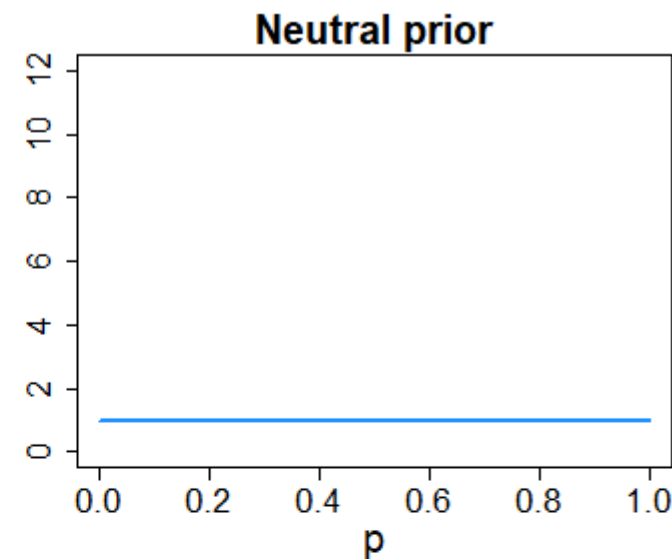
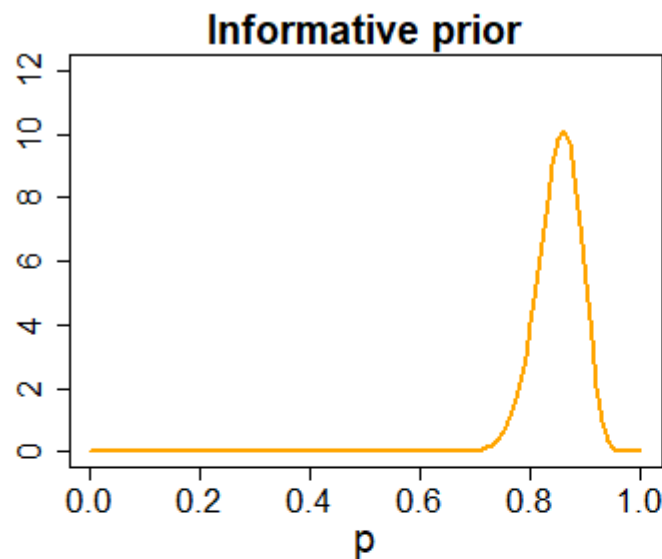
**Risk:** In case of **conflict**, a too informative prior can **increase the chance of making wrong conclusions (!)**



# Robustification: get prepared for the unexpected

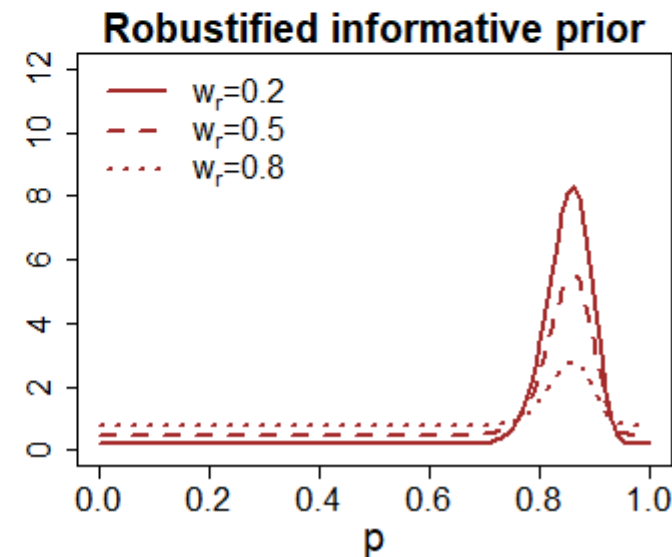
**Solution<sup>1</sup>:** *mix* **informative** prior (from past data) with a **neutral** one

$$\pi_R(p) = w_r \pi_1(p) + (1 - w_r) \pi_0(p)$$



$w_r \in [0, 1]$  reflects how much we rely on past data

The smaller  $w_r$ , the less rely on the past  
...but the potential of Bayesian approach is reduced (!)



# Self-Adapting Mixture (SAM) priors

SAM prior<sup>2</sup> dynamically adapts the level of borrowing from historical prior based on the *degree of consistence* between historical ( $D_h$ ) and new data ( $D$ ).

$$p \sim \tilde{w} \cdot \pi_1(\theta) + (1 - \tilde{w}) \cdot \pi_0(\theta)$$

informative prior based on  $D_h$  and with mean  $\theta_h$  ↖ Uniform[0,1]

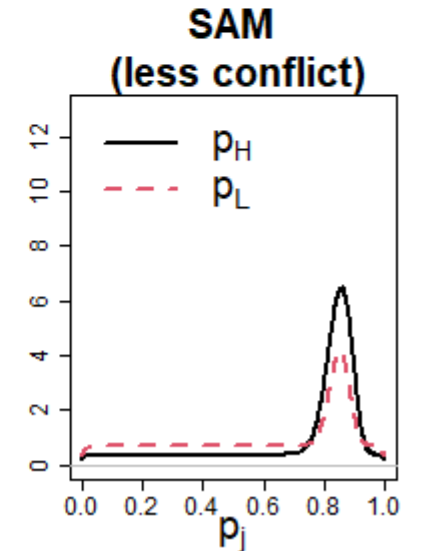
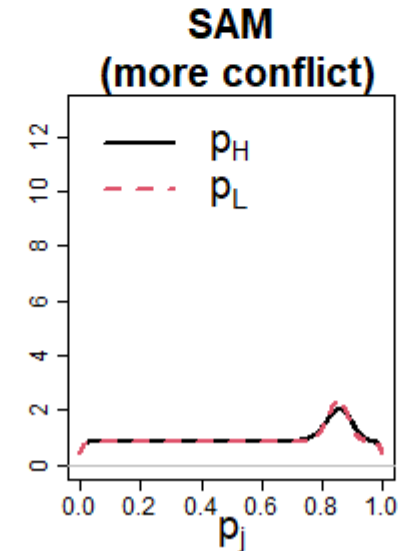
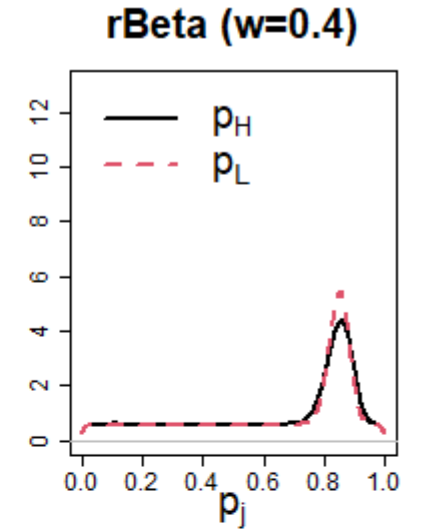
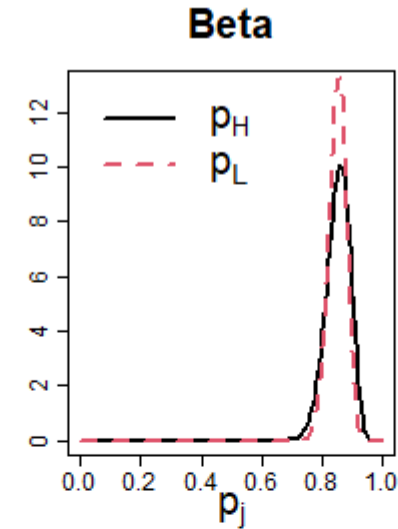
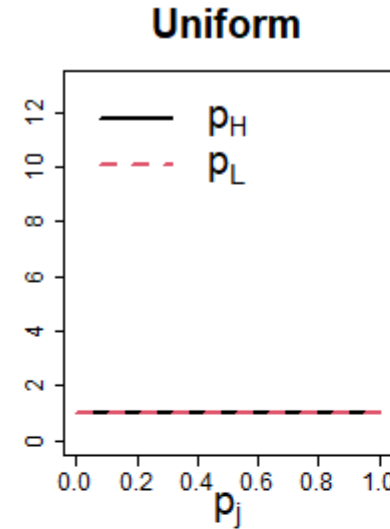
If  $H_0: \theta = \theta_h$  ( $D$  and  $D_h$  **consistent**) and  $H_1: \theta = \theta_h \pm 0.05$  ( $D$  and  $D_h$  in **conflict**), then

$$\tilde{w} \propto \frac{L_\theta(D|H_0)}{L_\theta(D|H_1)} = \frac{L_\theta(D|\theta = \theta_h)}{\max\{L_\theta(D|\theta = \theta_h \pm 0.05)\}}$$

**The larger the conflict between  $D$  and  $D_h$ , the less the borrowing from  $D_h$**

# Prior specifications (example)

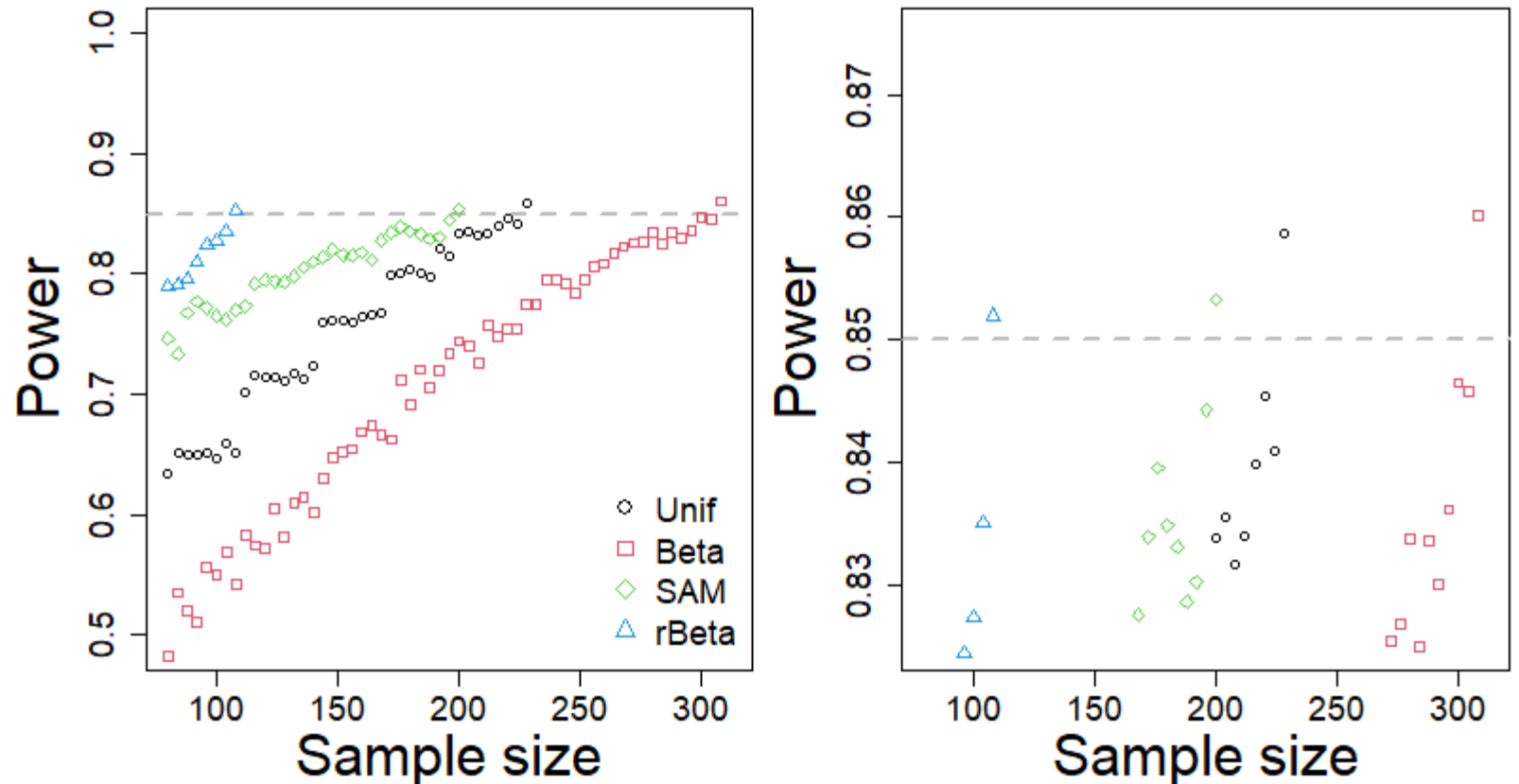
- **Uniform:**  $p_H, p_L \sim \text{Unif}[0,1]$
- **Beta:**  $p_H \sim \text{Beta}(\text{mean} = \hat{p}_j^H, \text{sd} = 0.04)$   
 $p_L \sim \text{Beta}(\text{mean} = \hat{p}_j^H, \text{sd} = 0.03)$   
with  $\hat{p}_j^H = 0.85$  historical survival rate
- **rBeta:**  $p_j \sim w \cdot \text{Beta}_j + (1 - w) \cdot \text{Unif}$ ,  $w = 0.4$ ,  $j = \{H, L\}$
- **SAM:** same as rBeta but with **dynamic** weight  $w_j$  determined by the level of prior-data conflict  
(N.B. the larger  $|\hat{p}_j - \hat{p}_j^H|$ , the larger the conflict)



# Sample size determination

- Forward search on grid of sample sizes ( $n_C = n_L = n/2$ )
- Stop when target power (85%) is achieved
- $\xi$  calibrated to control  $\alpha = 20\%$  under  $H_0: p_H = 0.75, p_L = 0.65$

$H_1: p_H = 0.8, p_L = 0.8$  (Zoom in)



Results based on 50k posterior samples  
for each of the 200k replicas



# Sample size determination

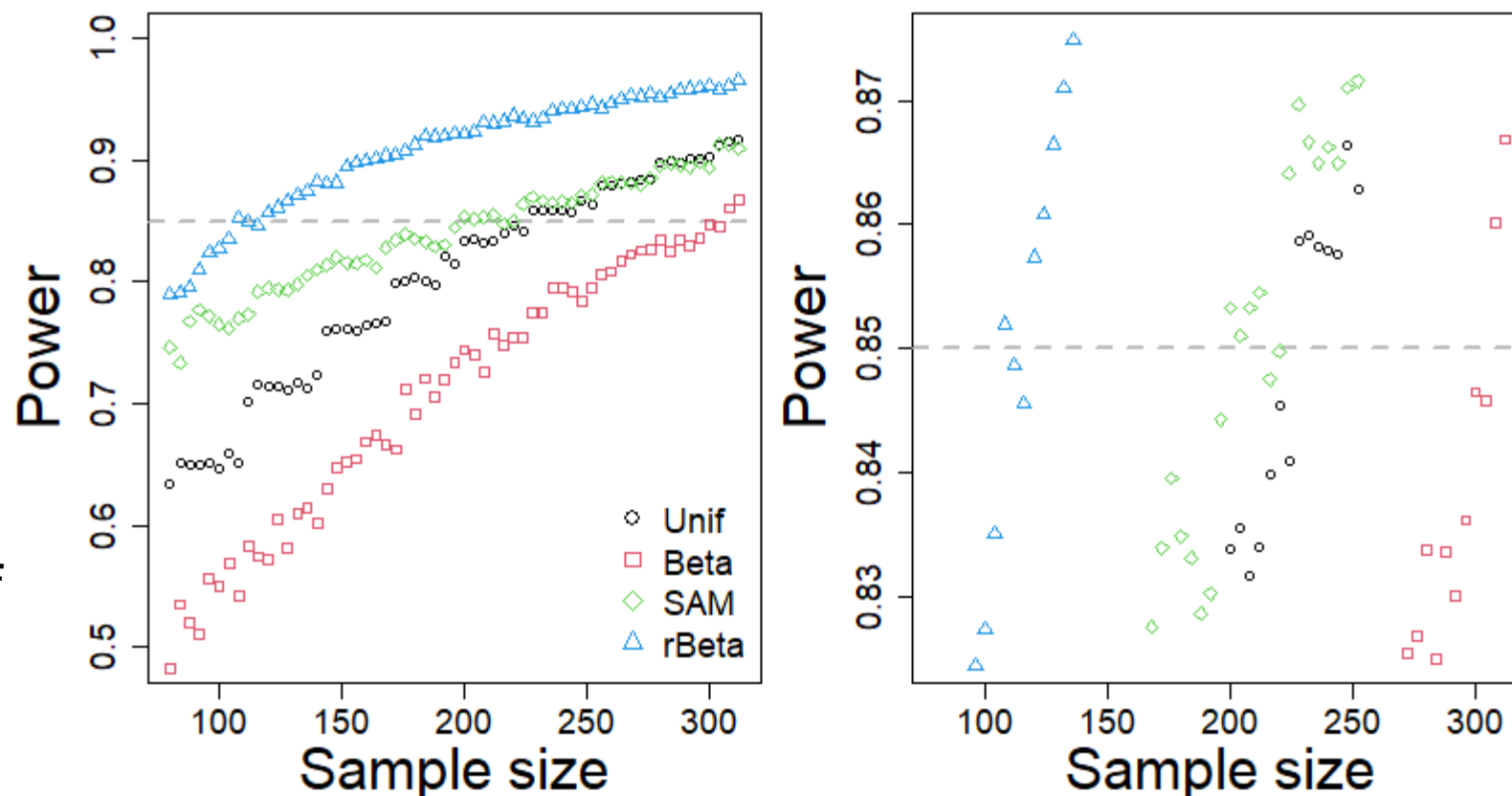
## Caution:

Estimated power may decrease with sample size (simulation error?)



Counterintuitive conclusion if we only rely on the power for a specific sample size

$H_1: p_H = 0.8, p_L = 0.8$  (Zoom in)



# Sample size determination

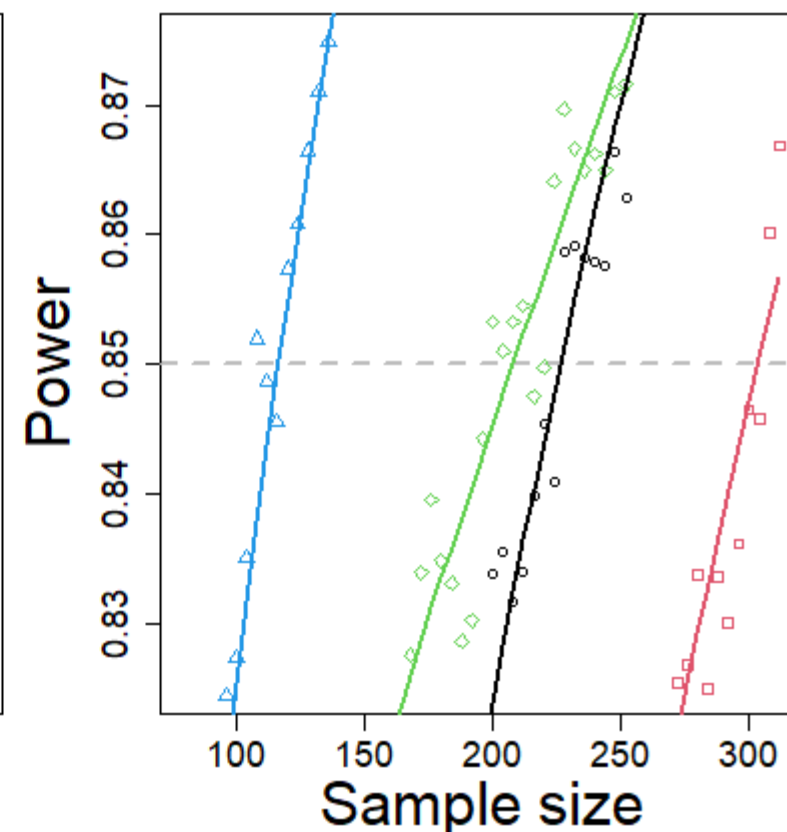
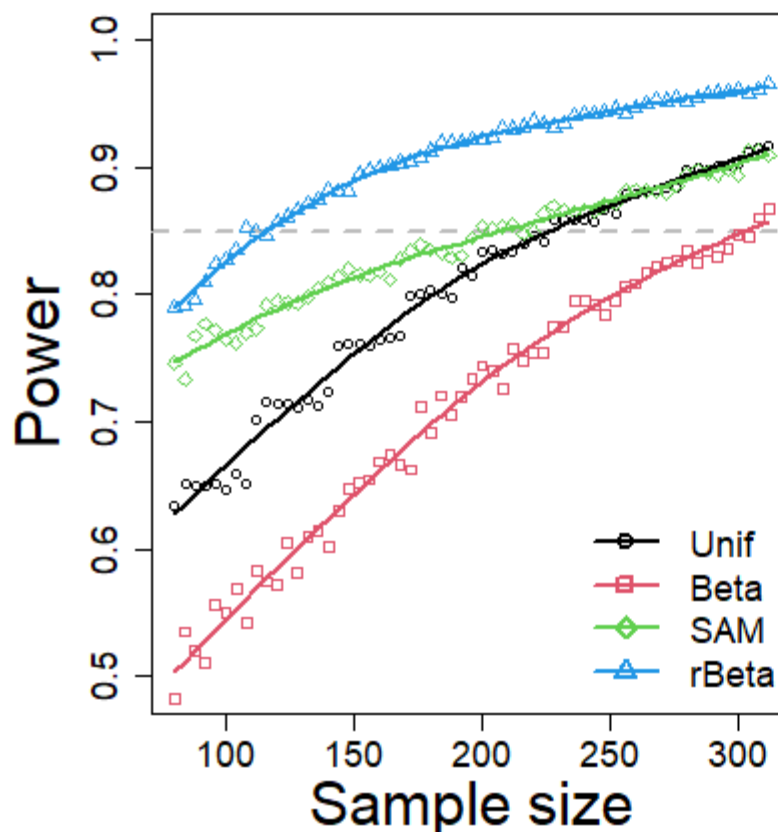
## Solution:

Non-parametric regression  
to fit smooth power curve



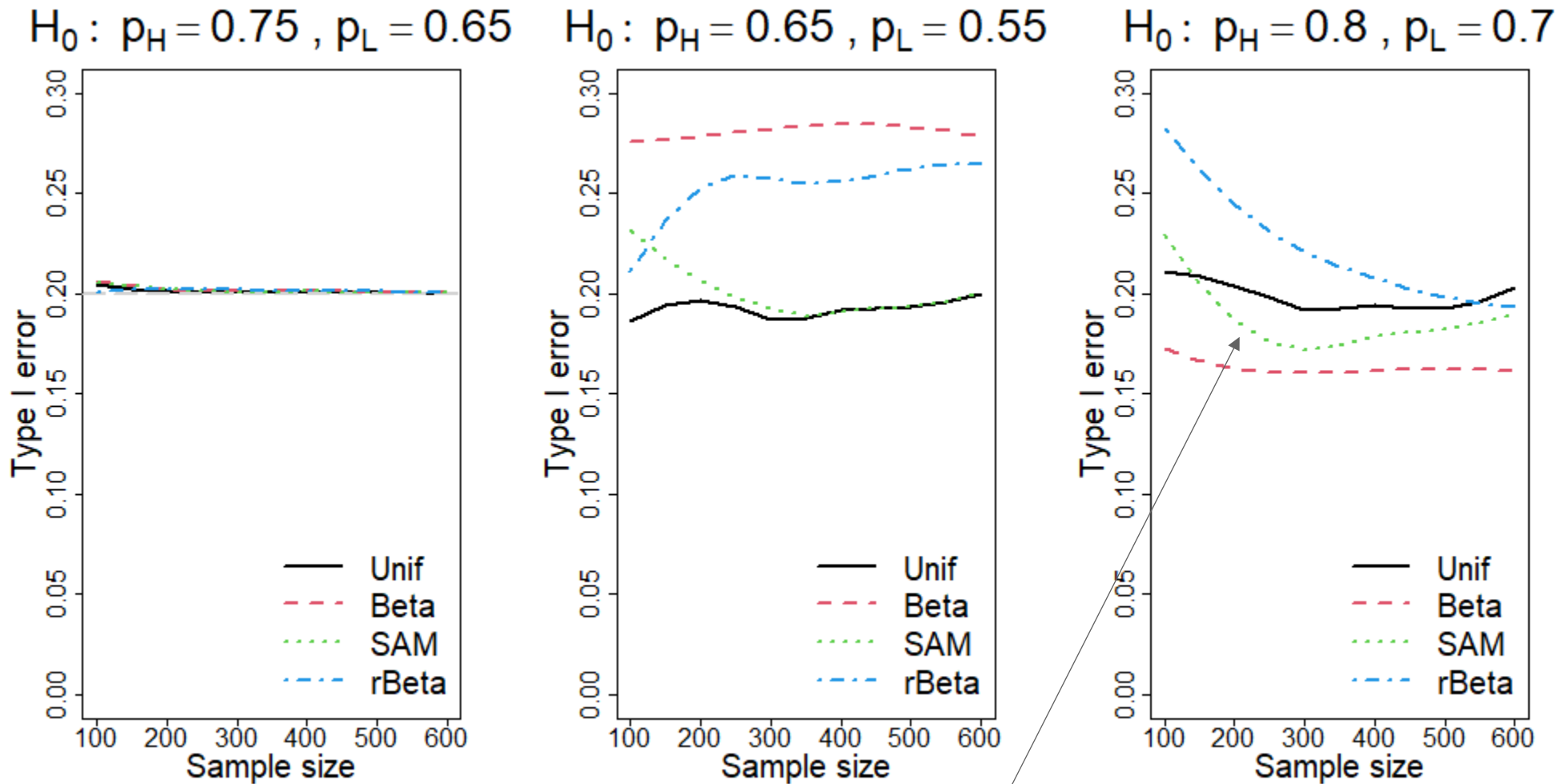
More coherent  
interpretation of power vs  
sample size relationship

$H_1: p_H = 0.8, p_L = 0.8$  (Zoom in)

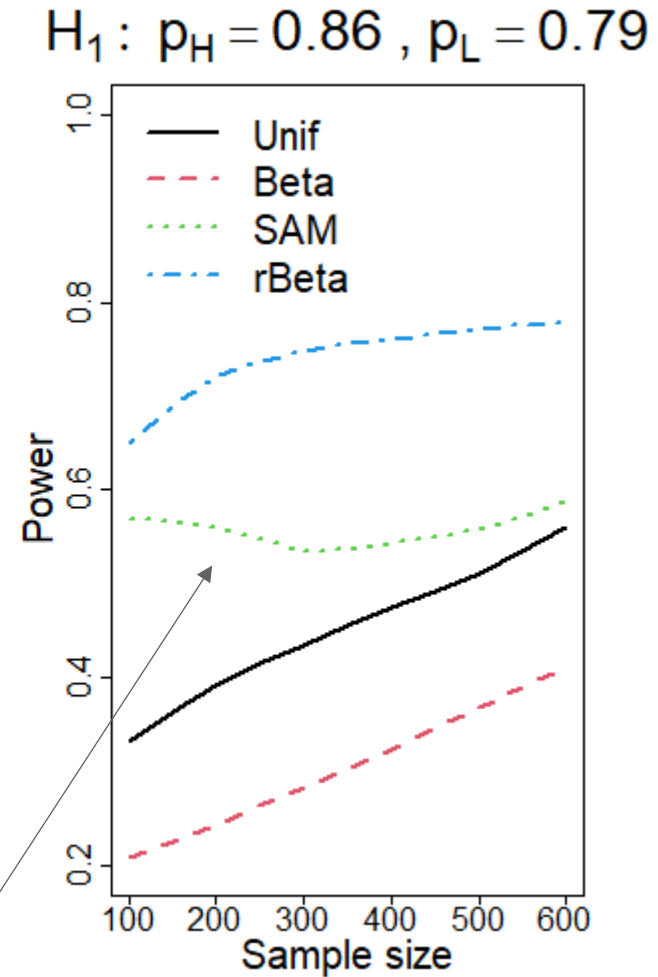
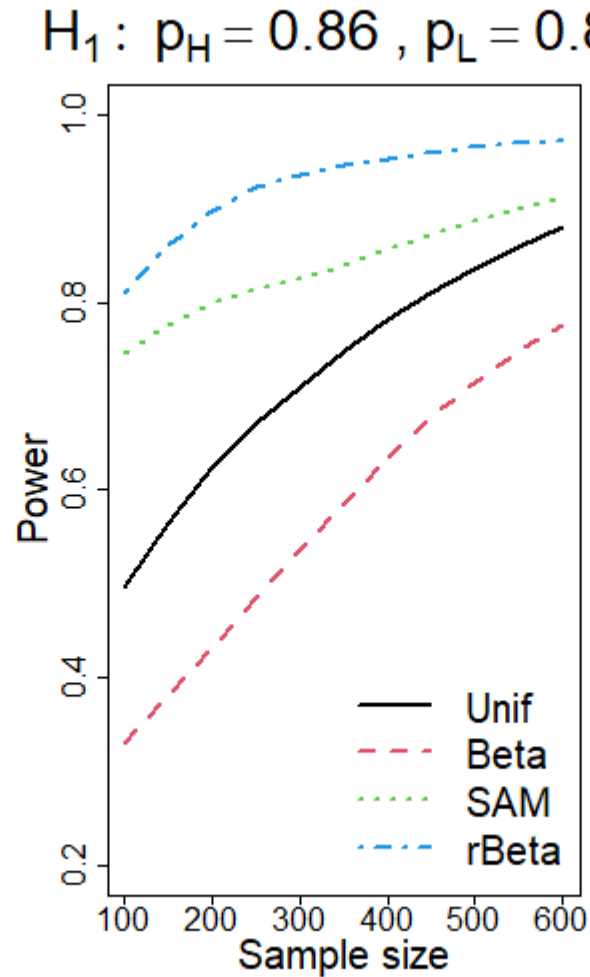
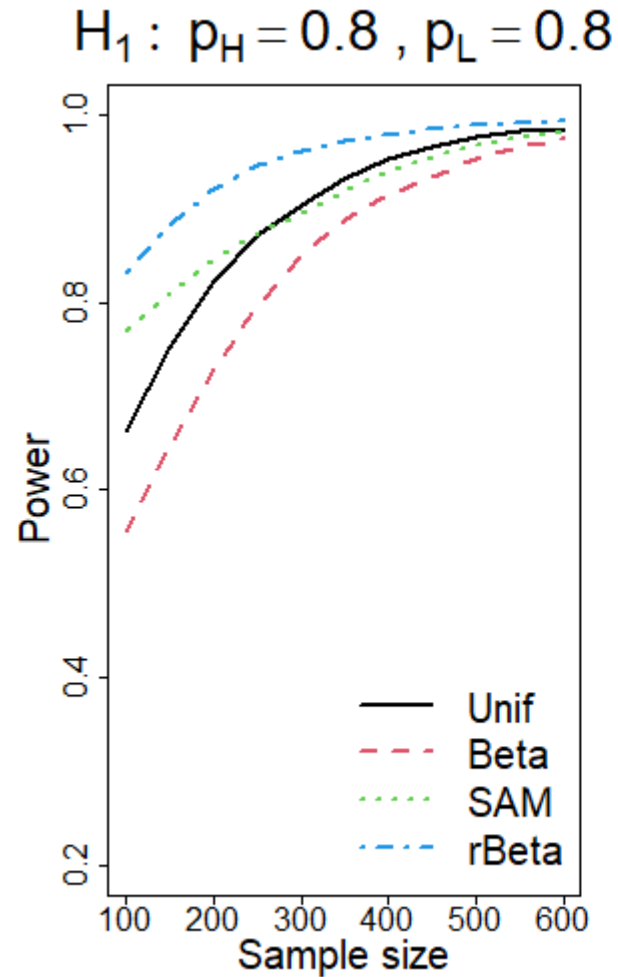


What if the overall trend itself  
is non-monotonic?

# Type-I error rates



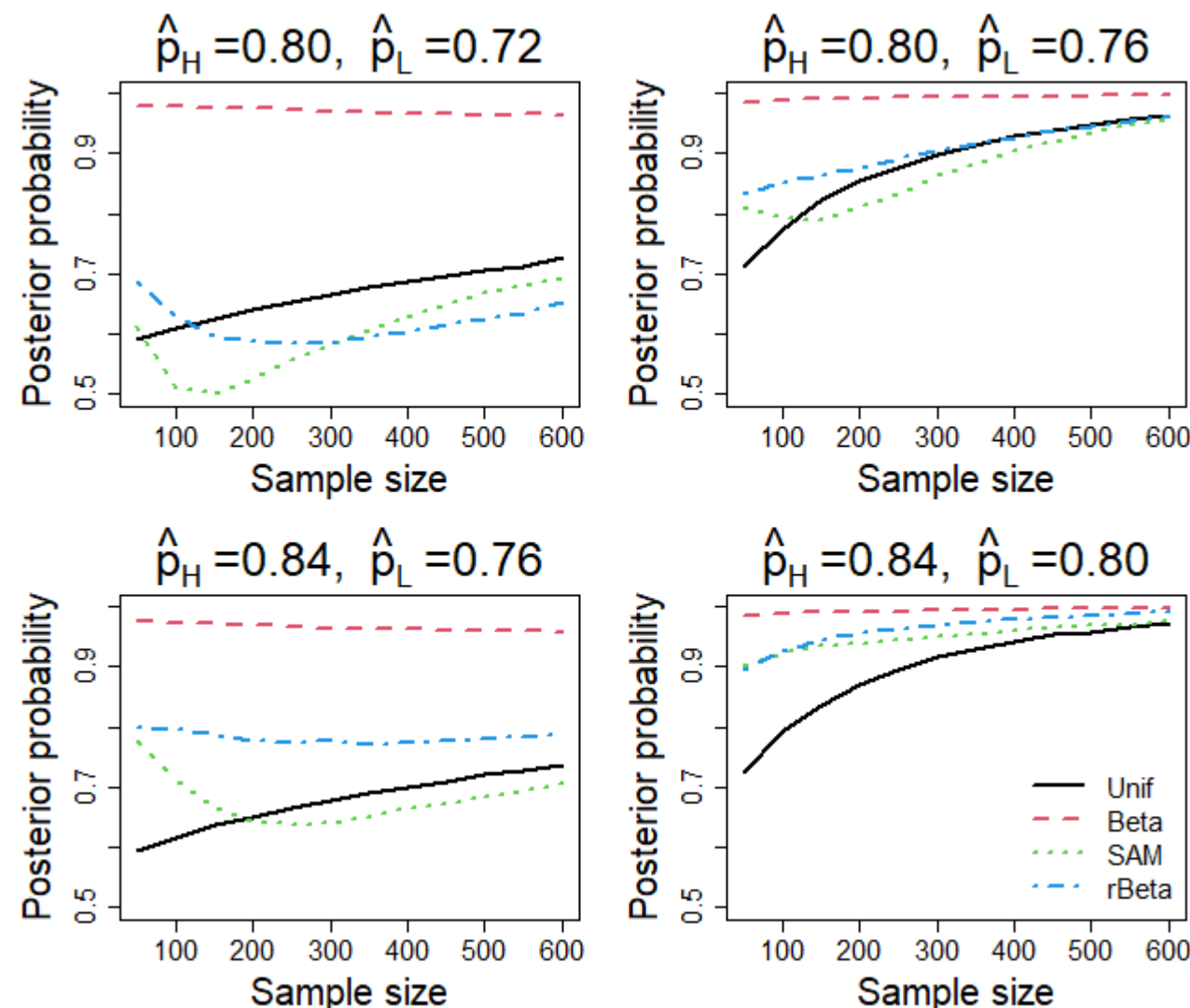
# Power



# Closer look at posterior probability of $H_0$ being false

For fixed observed response rates  $(\hat{p}_H, \hat{p}_L)$ , posterior probability that  $H_0$  is false based on SAM prior shows **evident non-monotonic behaviour** with sample size

Similar result obtained by Kopp-Schneider et al. (2020) on single-arm trial, with posterior probability decreasing with number of responses



# Final remarks

Dynamic borrowing of historical information allows for **prompt reaction to prior-data conflict**, by discounting the amount of information borrowed

...but **careful use is needed**:

- Bayesian **principle of independence** between prior and data is **violated**
- In some scenarios, the conflict between informative prior component and data may lead to **power curves that are non-monotonic with sample size**
- Sensitivity analysis for different sample sizes may be needed, above all **if more patients than expected are recruited**

# Main references

Schmidli, H., Gsteiger, S., Roychoudhury, S., O'Hagan, A., Spiegelhalter, D., & Neuenschwander, B. (2014). Robust meta-analytic-predictive priors in clinical trials with historical control information. *Biometrics*, 70(4).

Yang, P., Zhao, Y., Nie, L., Vallejo, J. & Yuan, Y. (2023). SAM: Self-adapting mixture prior to dynamically borrow information from historical data in clinical trials. *Biometrics*, 79(4).

Kopp-Schneider A, Calderazzo S, Wiesenfarth M. (2020). Power gains by using external information in clinical trials are typically not possible when requiring strict type I error control. *Biometrical Journal*, 62(2).





MRC  
Biostatistics  
Unit



UNIVERSITY OF  
CAMBRIDGE

**Thank you for your attention!**